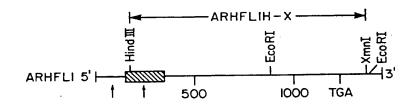
FIGURE 1

```
Α.
                                                                                     AG-3' (100%)
                                                        AAG
                                                                          TTC
                                                              GTC
                                                                    TTC
                                                                                AAA
                                             GGC
                                                   TGT
Oligo A Complement
                                  TGT
                                       GAG
                                                              ***
                                                                    ***
                                                                          ***
                                              *
                                                   **
                                                                          TTC
                                                                                     AG
                                                                                              (84%)
                                                                                AAA
                                                              GTC
                                                                    TTC
                            ACA
                                       GGA
                                             AGC
                                                   TGC
                                                         AAG
                                  TGT
hAR
                                                                                              (88%)
                                                                                AAG
                                                                                     AG
                                                   TGT
                                                         AAG
                                                              GTC
                                                                    TTC
                                                                          TTT
     (11)
                                       GGG
                                             AGC
                            ACC
                                  TGT
hPR
                                                                                              (81%)
                                                                          TTC
                                                                                AAA
                                                                                     AG
                                                              GTT
                                                                    TTC
                            ACC
                                                   TGC
                                                         \mathbf{A}\mathbf{A}\mathbf{A}
                                  TGT
                                        GGC
                                             AGC
hMR
     (4)
                                                                                              (81%)
(91%)
                                                                                AAA
                                                                                     AG
                                                                    TTC
                                                                          TTC
                                             AGC
                                                   TGT
                                                         AAA
                                                              GTT
                            ACT
                                  TGT
                                       GGA
hGR
     (5)
                                                                                     AG
hER (6)
hT3R (3, 17)
                                                   TGT
                                                         AAG
                                                              GCC
                                                                    TTC
                                                                          TTC
                                                                                AAG
                                  TGT
                                       GAG
                                             GGC
                            TCC
                                                              GGT
                                                                    TTC
                                                                          TTT
                                                                                AGA
                                                                                     AG
                                                                                              (78%)
                                                   TGC
                                                         AAG
                            ACG
                                  TGT
                                        GAA
                                             GGC
                                                                                              (78%)
                                                                                     CG
                                                                    TTC
                                                                          TTC
                                                                                CGC
                                       GAG
                                             GGC
                                                   TGC
                                                         AAG
                                                              GGC
                            GCC
                                  TGT
hRAR (17)
```

В.

C.

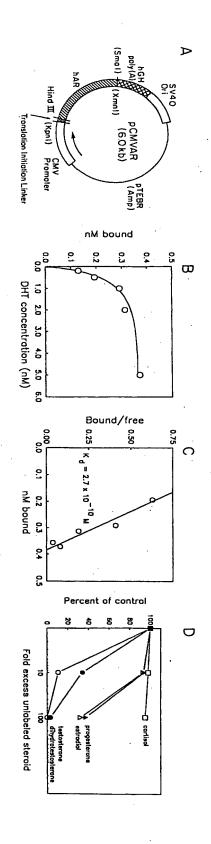


DNA-Binding Domain

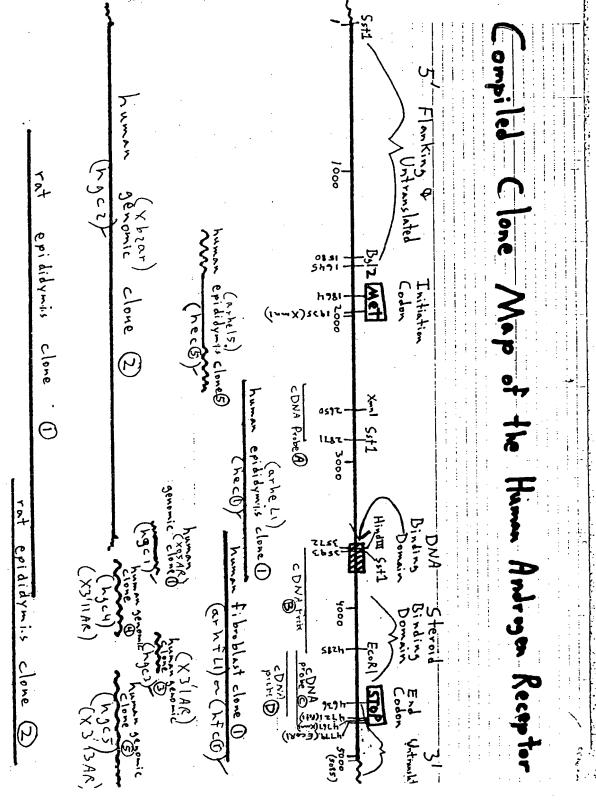
			+			+						10)							+		20)+									31	,		
hAR			Ċ	L	1	C	G	D	E	Α	s	G	С	н	Y	G	Α	L	T	С	G	S	С	K	V	F	F	ĸ	R	Α	A	E	G	(100	₹)
hPR		567)	Č	L	ī	Ċ	G	D	E	Α	s	G	С	н	Y	G	ν	L	T	С	G	S	С	K	v	F	F	K	R	Α	M	E	G	(94	8)
hMR	•	603)	Ċ	L	v	C	G	D	E	Α	S	G	С	н	Y	G	v	v	T	С	G	S	С	K	ν	F	F	K	R	Α	V	E	G	(87	8)
hGR	•	421)	Ċ	L	v	C	s	D	E	A	S	G	С	Н	Y	G	v	L	T	С	G	S	С	K	ν	F	F	K	R	Α	ν	E	G	(87	8)
hER	•	185)	C	Ā	v	С	N	D	Y	Α	S	G	Y	Н	Y	G	ν	W	s	С	E	G	С	K	Α	F	F	ĸ	R	S	I	Q	G	(55	₹)
cVDR	,		Č	G	v	С	G	D	R	Α	Т	G	F	н	F	N	Α	M	T	С	E	G	С	K	G	F	F	R	R	S	М	K	R	(48	8)
hT3R	(aa	102)	C	v	ν	С	G	D	ĸ	Α	T	G	Y	Н	Y	R	С	1	T	С	E	G	С	K	G	F	F	R	R	T	I	Q	K	(48	8)
vERBA	•	•	C	v	v	C	G	D	ĸ	Α	Т	G	Y	Н	Y	R	С	1	T	С	E	G	С	K	S	F	F	R	Ŕ	T	I	Q	K	(48	8)
hRAR	•		C	F	V	C	Q	D	K	S	S	G	Y	Н	Y	G	V	S	A	С	E	G	С	ĸ	G	F	F	R	R	S	I	Q	K	(45	8)

	+	40 +	50 +	+ 60+ ·	
hAR	KOKYLĆA	SRNDCTIDK	FRRKNCPS	CRLRKCYEAG	4 (100%)
hPR	OHNYLCA	GRNDCIVDK	IRRKNCPA	CRLRKCCQAGI	M (71%)
hMR	OHNYLCA	GRNDCIIDK	IRRKNCPA	CRLQKCLQAG	M (71%)
hGR	OHNYLCA	GRNDCIIDK	IRRKNCPA	CRYRKCLQAG	M (71%)
hER				CRLRKCYEVG	
cVDR	KAMFTCP	FNGDCKITK	DNRRHCQA	CRLKRCVDIG	M (40%)
hT3R	NLHPSYSCK	YEGKCVIDK	VTRNQCQE	CRFKKCIYVG	M (40%)
VERBA	NLHPTTSCT	YDGCCVIDK	ITRNQCQL	CRFKKCISVG	M (37%)
hRAR	NMVYTCH	RDKNCIINK	VTRNRCQY	CRLQKCFEVG	4 (43%)

.....



16UKE 1



= Unsequenced

FIGURE 4 (page 1 of 6)

10	20	30	40	50	60
GAGCTCTGGA	CAAAATTGAG	CGCCTATGTG	TACATGGCAA	GTGTTTTTAG	TGTTTGTGTG
CTCGAGACCT	GTTTTAACTC	GCGGATACAC	ATGTACCGTT	CACAAAAATC	ACAAACACAC
70	80	90	100	110	120
TTTACCTGCT	TGTCTGGGTG	ATTTTGCCTT	TGAGAGTCTG	GATGAGAAAT	GCATGGTTAA
AAATGGACGA	ACAGACCCAC	TAAAACGGAA	ACTCTCAGAC	CTACTCTTTA	CGTACCAATT
130 AGGCAATTCC TCCGTTAAGG	140 AGACAGGAAG TCTGTCCTTC	150 AAAGGCAGAG TTTCCGTCTC	AAGAGGGTAG TTCTCCCATC	170 AAATGACCTC TTTACTGGAG	180 TGATTCTTGG ACTAAGAACC
190	200	210	220	230	CCCTATGACG
GGCTGAGGGT	TCCTAGAGCA	AATGGCACAA	TGCCACGAGG	CCCGATCTAT	
CCGACTCCCA	AGGATCTCGT	TTACCGTGTT	ACGGTGCTCC	GGGCTAGATA	
250	260	270	280	290	300
GAACTCTAAG	GTTTCAGCAT	CAGCTATCTG	CTGGCTTGGT	CACTGGCTTG	CCTCCTCAGT
CTTGAGATTC	CAAAGTCGTA	GTCGATAGAC	GACCGAACCA	GTGACCGAAC	GGAGGAGTCA
310	320	330	340	350	360
TTGTAGGAGA	CTCTCCACT	CTCCCATCTG	CGCGCTCTTA	TCAGTCCTGA	AAAGAACCCN
AACATCCTCT	GAGAGAGGTGA	GAGGGTAGAC	GCGCGAGAAT	AGTCAGGACT	TTTCTTGGGN
370	380	390	400	410	420
TGGCNAGCCA	GGAGCNAGGT	ATTCNTATCG	TCCTTTTCNT	CCTCCTNGCC	TCACCTNGTT
ACCGNTCGGT	CCTCGNTCCA	TAAGNATAGC	AGGAAAAGNA	GGAGGANCGG	AGTGGANCAA
430	440	450	460	470	480
GNTTTTTAGA	TTGGNCTTNG	NAACCAAATT	TGTATGCTGG	CCTCCAGGAA	ATCTGGAGCC
CNAAAAATCT	AACCNGAANC	NTTGGTTTAA	ACATACGACC	GGAGGTCCTT	TAGACCTCGG
490	500	510	520	530	540
TGBCGCCTAA	ACCTTGGTTT	AGGAAAGCAG	GAGCTATTCA	GGAAGCAGGG	TCCTCCAGGG
ACCGDGGATT	TGGAACCAAA	TCCTTTCGTC	CTCGATAAGT	CCTTCGTCCC	AGGAGGTCCC
550	550	570	580	590	CCAAAGCNAC
CTAGAGCTAG	CCTCTCCTGC	CCTCGCCCAC	GTGCGCCAGC	ACTTGTTTCT	
GATCTCGATC	GGAGAGGACG	GGAGCGGGTG	CACGCGGTCG	TGAACAAAGA	
610	620	630	640	650	660
TAGGCAGGCG	TTAGCGCGCG	GTGAGGGGAG	GGGAGAAAAG	GAAAGGGGAG	GGGAGGGAAA
ATCCGTCCGC	AATCGCGCGC	CACTCCCTC	CCCTCTTTTC	CTTTCCCCTC	CCCTCCCTTT
670 AGGAGGTGGG TCCTCCACCC	680 AAGGCAAGGA TTCCGTTCCT	690 GGCCGGCCNG CCGGCCGGNC	GTGGGGGGGG	GACCCGACTC	720 GCANNAACTG CGTNNTTGAC
730 TTGCATTTGC AACGTAAACG	TOTOCACCTO	750 CCAGCGCCCC GGTCGCGGGG	CTCCGAGATC	CCGGGGGAGCC	780 AGCTTGCTGG TCGAACGACC
790 GAGAGCGGGA CYCTCGCCCT	ACGGTCCGGA	810 GCAAGCCCAG CGTTCGGGTC	AGGCAGAGGA	GGCGACAGAG	840 GGAAAAAGGG CCTTTTTCCC
028 CCCNAGCTAG GGGNTCGATC	CCGCTCCAGT	GCTGTACAGN CGACATGTCN	AGCCGAAGGA	CGCACCACGC	900 CAGCCCCAGC GTCGGGGTCG

F164RE 4 (page 2 of 6)

	910	920	930	940	950	960
	CCGGCTCCAG	CGACAGCNAA	CGCCTCTTGC	ANGCGTTCGA	AGCCGCCGCC	CGGAGCTGCC
	GGCCGAGGTC	GCTGTCGNTT	GCGGAGAACG	TNCGCAAGCT	TCGGCGGCGG	GCCTCGACGG
	970	980	990	1000	1010	1020
	CTTTCCTCTT	CGGTGAAGTT	TTTAAAAGCT	GCTAAAGACT	CGGAGGAAGC	AAGGAAAGTG
	GAAAGGAGAA	GCCACTTCAA	AAATTTTCGA	CGATTTCTGA	GCCTCCTTCG	TTCCTTTCAC
	1030 CCTGGTAGGA GGACCATCCT	1040 CTGACGGCTG GACTGCCGAC	1050 CCTTTGTCCT GGAAACAGGA	1060 CCTCCTCTCC GGAGGAGAGG	ACCCCGCCTC	1080 CCCCCACCCT GGGGGTGGGA
	1090	1100	1110	1120	1130	1140
	GCCTTCCCCC	CCTCCCCGT	CTTCTCTCCC	GCAGCTGCCT	CAGTCGGCTA	CTCTCAGCCA
	CGGAAGGGGG	GGAGGGGGCA	GAAGAGAGGG	CGTCGACGGA	GTCAGCCGAT	GAGAGTCGGT
	1150	1160	1170	1180	1190	1200
	ACCCCCCȚCA	CCACCCTTCT	CCCCACCGC	CCCCCCCCC	CCGTCGGCCC	AGCGNTGNCA
	TGGGGGGAGT	GGTGGGAAGA	GGGGTGGGCG	GGGGGGGGGG	GGCAGCCGGG	TCGCNACNGT
	1210	1220	1230	1240	1250	1260
	GNCCGAGTTT	GCAGAGAGGT	AACTCCCTTT	GGCTGCGAGC	GGGCGAGNCT	AGCTGCACAT
	CNGGCTCAAA	CGTCTCTCCA	TTGAGGGAAA	CCGACGCTCG	CCCGCTCNGA	TCGACGTGTA
	1270	1280	1290	1300	1310	1320
	TGCAAAGAAG	GCTCTTAGGA	GCAGGCGACT	GGGGAGCGGC	TTCAGCACTG	CAGCCACGAC
	ACGTTTCTTC	CGAGAATCCT	CGTCCGCTGA	CCCCTCGCCG	AAGTCGTGAC	GTCGGTGCTG
~	1330	1340	1950	1360	1370	1380
	CNGCCTGSTT	AGGCTGCACG	CGGABAGAAC	CCTCTGTTTT	CCCCCACTCT	CTCTCCACCT
	GNCGGACCAA	TCCGACGTGC	GCCTCTCTTG	GGAGACAAAA	GGGGGTGAGA	GAGAGGTGGA
	1390	1400	1410	1420	1430	1440
	CCTCCTGCCT	TCCCCACCCC	GAGTGCGGAG	CCAGAGATCA	AAAGATGAAA	AGGCAGTCAG
	GGAGGACGGA	AGGGGTGGGG	CTCACGCCTC	GGTCTCTAGT	TTTCTACTTT	TCCGTCAGTC
	1450 GTCTTCAGTA CAGAAGTCAT	1460 GCCAAÁAAAC CGSTTTTTTG	1470 AAAACAAACA TTTTGTTTGT	1480 AAAACAAAA TTTTGTTTTT	1490 AGCCGAAATA TCGGCTTTAT	AAAGAAAAAG
	1510	1520	1530	1540	1550	1560
	ATAATAACTC	AGTTCTTATT	TGCACCTACT	TCAGTGGACA	CTGAATTTGG	AAGGTGGAGG
	TATTATTGAG	TCAAGAATAA	ACGTGGATGA	AGTCACCTGT	GACTTAAACC	TTCCACCTCC
	1570	1580	1590	1600	1610	1620
	ATTTTGTTTT	TTTCTTTTAA	GATCTGGGCA	TCTTTTGAAT	CTACCCTTCA	AGTATTAAGA
	TAAAACAAAA	AAAGAAAATT	CTAGACCCGT	AGAAAACTTA	GATGGGAAGT	TCATAATTCT
	1630 GACAGACTGT CTGTCTGACA	1640 GAGCCTAGCA CTCGGATCGT	GGGCAGATCT	1660 TGTCCACCGT ACAGGTGGCA	GTGTCTTCTT	CTGCACGAGA
	1690 CTTTGAGGCT GAAACTCCGA	GTCAGAGCGC	TTTTTGCGTG	GTTGCTCCCG	1730 CAAGTTTCCT GTTCAAAGGA	1740 TCTCTGGAGC AGAGACCTCG
	1750 TTCCCGCAGG AAGGGCGTCC	TGGGCAGCTA	GCTGCAGCGA CGACGTCGCT	1780 CTACCGCATC GATGGCGTAG	ATCACAGCCT TAGTGTCGGA	GTTGAACTCT CAACTTGAGA
	4					

F16,4RE 4 (page 3 of 6)

1810	1820	1830	1840	1850	1860
TCTGAGCAAG	AGAAGGGGAG	GCGGGGTAAG	GGAAGTAGGT	GGAAGATTCA	GCCAAGCTCA
AGACTCGTTC	TCTTCCCCTC	CGCCCCATTC	CCTTCATCCA	CCTTCTAAGT	CGGTTCGAGT
1870	1880	1890	1900	1910	1920
AGGATGGAAG	TGCAGTTAGG	GCTGGGAAGG	GTCTACCCTC	GGCCGCCGTC	CAAGACCTAC
TCCTACCTTC	ACGTCAATCC	CGACCCTTCC	CAGATGGGAG	CCGGCGGCAG	GTTCTGGATG
1930	1940	1950	1960	1970	1980
CGAGGAGCTT	TCCAGAATCT	GTTCCAGAGC	GTGCGCGAAG	TGATCCAGAA	CCC666CCCC
GCTCCTCGAA	AGGTCTTAGA	CAAGGTCTCG	CACGCGCTTC	ACTAGGTCTT	666CCC6666
1990	2000	2010	2020	2030	2040
AGGCACCCAG	AGGCCGCGAG	CGCACCT	CCC66060CA	GTTTGCTGCT	GCTGCAGCAG
TCCGTGGGTC	TCCGGCGCTC	GCGTCGTGGA	T66080000	CAAACGACGA	CGACGTCGTC
2050	2060	2070	2080	2090	2100
CAGCAGCAGC	AGCAGCAGCA	GCAGCAGCAG	CAGCAGCAGC	AGCAGCAGCA	GCAGCAGCAG
GTCGTCGTCG	TCGTCGTCGT	CGTCGTCGTC	GTCGTCGTCG	TCGTCGTCGT	CGTCGTCGTC
2110	2120	2130	2140	2150	2160
CAGCAGCAAG	AGACTAGCCC	CAGGCAGCAG	CAGCAGCAGC	AGGGTGAGGA	TGGTTCTCCC
GTCGTCGTTC	TCTGATCGGG	GTCCGTCGTC	GTCGTCGTCG	TCCCACTCCT	ACCAAGAGGG
2170	2180	2190	2200	2210	2220
CAAGCCCATC	GTAGAGGCCC	CACAGGCTAC	CTGGTCCTGG	ATGAGGAACA	GCAACCTTCA
GTTCGGGTAG	CATCTCGGG	GTGTCCGATG	GACCAGGACC	TACTCCTTGT	CGTTGGAAGT
0825	2240	2250	2260	2270	2280
CAGCCCACA	CGGCCCTGGA	GTGCCACCC	GAGAGAGGTT	GCGTCCCAGA	GCCTGGAGCC
ACTECOBCCTC	GCCGGGACCT	CACGGTGGGG	CTCTCTCAA	CGCAGGGTCT	CGGACCTCGG
2290	2300	2310	2320	2330	2340
BCCGTGSCCB	CCAGCAAGGG	GCTGCCGCAG	CAGCTGCCAG	CACCTCCGA	CBABBATGAC
CGGCCACCGGC	CCCTTGCTGG	CGACGGCGTC	GTCGACGGTC	6TGGAGGCCT	BCTCCTACTG
0255 CCCCTOBACT BBBCARDTBA	2360 CATCCACGTT GTAGGTGCAA	2370 GTCCCTGCTG CAGGGACGAC	0865 0865 0865 0865 0865 0865	TECESGETT	2400 AAGCAGCTGC TTCGTCGACG
2410	2420	2430	2440	2450	2460
TCCGCTGACC	TTAAAGACAT	CCTGAGCGAG	GCCAGCACCA	TGCAACTCCT	TCAGCAACAG
AGGCGACTGB	AATTTCTGTA	GGACTCGCTC	CGGTCGTGGT	ACGTTGAGGA	AGTCGTTGTC
2470 CAGCAGGAAG GTCGTCCTTC	2480 CAGTATCCGA GTCATAGGCT	2490 AGGCAGCAGC TCCGTCGTCG	2500 AGCGGGAGAG TCGCCCTCTC	CGAGGGAGGC	CTCGGGGGGCT
0539 CCCACTTCCT ADDAADDAA	CCAAGGACAA	TTACTTAGGG	2560 GGCACTTCGA CCGTGAAGCT	CCATTTCTGA	CAACGCCAAG
2590 GAGTTGTGTA CTCAACACAT	AGGCAGTGTC	GGTGTCCATG	GGCCTGGGTG	TEGAGGCGTT	2640 GGAGCATCTG CCTCGTAGAC
2650 AGTCCAGGGG TCAGGTCCCC	AACAGCTTCG TTGTCGAAGC	GGGGGATTGC CCCCCTAACG	ATGTACGCCC	CACTTTTGGG GTGAAAACCC	AGTTCCACCC TCAAGGTGGG

FIGURE 4 (page 40f6)

100					
2760	2750	2740	2730	2720	2710
GCTAGACGAC	AAGGTTCTCT	GCCGAATGCA	TECCCCATTE	CCACTCCTTG	GCTGTGGCTC
CGATCTGCTG	TTCCAAGAGA	CGGCTTACGT	ACGGGGTAAC	GGTGAGGAAC	CGACACCGAG
2000 A	5546	88.00			
ني. 0282 ان 0282م	2810	2800	2790	2780	2770
AGGTTACACC	CITICAAGGG	GAGTATTUCC	AGATACTECT	AGAGCACTGA	AGCECAGGCA
ILLHH IDI DO	BHHHBIILLL	LICAIAABBB	TUTATUACUA	TOTOGTGAGT	TOGCGTCCGT
2880	2870	2860	2850	2040	555
GAGCTCCGGG			CCTACCCTCC	2840	0685
CTCBAGGCCC	CACCACCACC	ACACCETCEC	CCATCCCACC	AAGGLEAGAG	ARAGGGG TAG
CIDONOCCU	OHLO I LO I CC	HOHLLO I COL	BUAILLUALU	TICCOLICIC	THICECGATE
2940	2930	2920	2910	0098	2950
CGAGGCAGCT					
GCTCCGTCBA	CTESTSACET	ATGTTCAGGC	CCIGICICIC	ACCCOLCIME	TELLACTIONEE
1.5 m. 1.5 m.	CICO I DALCO	HIDI ICHODE	BOHLHBHBHB	HCBBCHBHIB	TE COMMETTE
3000	2990	2980	2970	2950	5950
GCCGCCCCT.		CCACTEBOTO			EPDOTACIONA DEGRACIONA
CGGCGGGGGA	ACCEBCCTES	GGTGACCGAG	GATGTTGAAA	CARCECTEAT	CCCATCGTCT
- X-X-		OB I EMBODINO	GATOTTONAN	CHOCCCTONT	COSMICCICI
3060	3050	3040	- 3030	3020	3010
CTACBGCABC -					COSCORDED
GATGCCGTCG	TGGGCGACCT	TTCGACCTCT	GCGAGCGTAG	GGGTAGGGGT	GGCGGCGGAG
3120,	3110	- 3100	3090	3080	2070
GCATEGCGCG CGTACCGCGC	TGGCGAGCCT	TATEGEGACC	GCACTGCCGC	CTAMEGGGGG	6001666066
CGTACCGCGC	ACCECTCEGA	A TACCCCTGG	ACGGO	9339337NB	COGACCEGEC
				4 91	
	3170	3160	3150	3140	3130
CTGGCACACT	CTTCCTCATC	TCAGCCGCCG	TEGETCACCC	GACCCGGTTC	
GACCGTGTGA	GAAGGAGTAG	AGTCGGCGGC	ACCCAGTGGG	CTGGGCCAAG	ADDAUGT0600
		3550	3210	3200	2190
GGGTGGTGGC	6166166166	GGACCGTGTG	CCAGTTGTAT	CCGAAGAAGG	CTCTTCASAG
CCCACCACCG	CACCACCACC	CCTGGCACAC	GGTCAACATA	GGCTTCTTCC	GAGAAGTGTC
3300	2250	6004	8884		
		9280	3270	3260	9250
CGAGGCGGGA		0000000000	06606666666	606606666	686666666
GCTCCGCCCT	LULLULLULL		GUUGUUGUUG	CRECEBECE	DUG A.B. A.B.
3360	3350	3340	3330	2224	2210
GGAAAGCGAC				9320	9310
CCTTTCGCTG		CCICAGGGGC	CACICOGCCC	COLUMNICATION	CCACATAGGG
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	DEAG (CCCC	GIBHOCCOSC	COMPOCEUM	CONCHICODO
3420	3410	3400	3390	3380	3370
CTATCCCAGT				CTGATGTGTG	TICADOSCAD
GATAGGGTCA:	CGTCTCACGG	CCGTACCACT	CATGGGACCG	BACTACACAC	AAGTGGCGTG
		3460	3450	3440	3430
GGAACCTTAC	GCTACTCCCG	TGGATGGATA	AATGGGCCCC	TCANAÁGCGA	DUCACTIGIG
CCTTGGAATG	CGATGAGGGC	ACCTACCTAT	TTACCCGGGG	AGITTTCGCT	GRETEAACAD
1					
					3470
TTACTTTCCA	CCATTGACTA	CATGTTTTGC	TGCCAGGGAC	GTTTGGAGAC	GEGGACATGO
AATGAAAGGT	GGTAACTGAT	GTACAAAACG	.ACGGTCCCTG	CAGADUTOTO	DODOT STADG
					3550
TEGAGCTCTC	GGTGTCACTA	GAAGCTTCTG	CTGTGGAGAT	CCTGCCTGAT	CCCLAGAAĞA
ACCTCGAGAG	CCACAGTGAT	CTTCGAAGAC	GACACCTCTA	GEACGGACTA	GGGGTCTTCT

FIGURE 4 (page 50 f 6)

GCTGTCATTC AGTACTCCTG GATGGGGCTC ATGGTGTTTG CACAGAAG CTCATGGAGAG CTCATGGAGAG CTCATGCAGAAAC CTCATGGAGAG CTCATGCAGAAAC CGGGAACAAAC GGTACCGAAAG CGGTACCGAAAG CGGGGACTAG ACCAAAAGTT AGAGTACCGC ACCCACAAAGTT AGAGTACCAAAAGTT AGAGTACCAAAAGTT AGAGTACCAAAAGTT AGAGTACCAAAAGTT AGAGTACCAAAAGTT AGAGTACCAAAAGTT AGAGTACCAAAAGTT AGAGTACAAAAAGTT AGAGAAAGTAAAAAAAAAA						
TEGECCASCA GAAATBATTE CACTATTGAT AAATTCGSA GGAAAAATTE TCCATCTTGT AGGTGGACA	GAAGTACCTG	AAGGGAAACA	AGAGCCGCTG	CTTCTTCAAA	GCTGCAAGGT	· ACATRICGAA
CBTCTITGESA AATSTTATGA ABCAGSGATE ACTCTEGSAG CCCGGAAGCT GAAGAACTT GAGAAACCCT TTACAATACT TCGTCCCTAC TBAGACCCTC GBGCCTTCGA CTTCTTTBAA GBTAATCTGA AACTACAGGA GBGAAGAGAG CCTTCCAGCA CCACCAGCCC CACTGAGGAG GBTAATCTGA AACTACAGGA GBGAAGAGAG CCTTCCAGCA CCACCAGCCC CACTGAGGAG 3850 3850 3850 3870 3880 3890 3900 ACACCACGA AACTGACAGAG CTTCACACTT GAAGGCTATGA CATCTTCGG CCACCAGCCC CATCTTTCG TGTTGGGACC TTCGGCACATT CAGCACACGAC CTTGACCACT GAACACACCAC CATCACACGCC CATCACACCAC CAACCACACCAC CATTGACCACACCACACACACACACACACACACACACACA	TCCATCTTGT	GGAAAAATTG	AAATTCCGAA	CACTATTGAT	GAAATGATTG	TROGCCAGCA
GSTAATCTGA AACTACAGGA CCTTCCTCTC CCTTCAGCT CCATCAGCC CACCAGCCC CACCAGCCCC CACCAGCCCCC CACCAGCCCCCCCCCC	GAAGAAACTT	CCCGGAAGCT	ACTCTGGGAG	AGCAGGGATG	AATGTTATGA	CGTCTTCGGA
ACAACCCAGA TGTTSGSTCT TCGACTGTCA 3910 3920 3930 3940 3970 AATGTCCTGG AAGCCATTGA TCGAGTGTAA 3970 GACTCCTTTG GACCATTGA CGGTCCACAT CGGTCACAC CGGTCTCTCT CGGACAGTGC CGGACAGGGC CTGCTCTCTC CGGACAGGGC CTGCTCTCTC CGGACAGGGC CTGCTCTCTC CGGACAGGGC CTGCTCTCTC CGGACAGGGC CTGCTCTCTC CGGACAGGGC CTGCTCTCC CGGACAGGGC CTGCTCTCC CGGACAGGGC CTGCTCTCC CGGACAGGGC CTGCTCTCC CGGACAGGGC CTGCTCTCC CGGACAGGGC CTGCTCACC CGGACAGGAC CTGCTCACC CGGACAGGAC CTGCTCACC CGGGGACTAC CGGGGACTAC CGGCTCACC CGGGGACTAC CGGGGACTAC CCGGGGACTAC CCGGGGGCTAC CCGGGG	CACTGAGGAG	CCACCAGCCC	GCTTCCAGCA	GGAAGGAGAG	AACTACAGGA	GGTAATCTGA
AATGTCCTGG AAGCCATGA CCGGTCACAT CACACAGAC CTGTGCTGTT GTTGGTCGGG 3970 3980 3990 4000 4010 4020 GCTCTCTTTG GTCGGAACAGA CAACCAGGAC CTGTGCTGTT CTGAGGAACACGAACAGAACA	CATCTTTCTG	AATGTCAGCC	GAAGGCTATG	GTCACACATT	AGCTGACAGT	ACAACCCAGA
GACTECTTTE CAGCCTTECT CTCTAGECTC GAGATGAG GAGAGAGACA GTTGTACAC CTGTGAGGAAAC GTCGGAACGA GAGACGAACA GTTGTACAC CTCTCTCTGT CGAACATGTG CACCAGATTCA CCCCGGTTCCC GAGACGGACCG TTCCCCAACT TACACGTGGA ATGTGCACCT ACCCCAGATTCA CCCCGGTTCCC GAACGGACCG AAGGCGTTGA ATGTGCACCT ACCCCAGATT ACCCCCAACT TACCACCAAAC GCTGCCCCAACT TACCACCAAAC GCTGCCCCAACT TACCACCAAAC GCTGCCCCAACT TACCACCAAAC GCTGCCCCAACT TACCACCAAAC GCTGCCCCAACT TACCACCAAAC GCTACCCCAAC TACCACCAAAC GCTACCCCGAACT TACCACCAAAAC GCTACCCCGAACT TACCACCAAAC GCTACCCCGAACT TACCACCAAAAC GCTACCCCCAAC GCCACCACAC GCCACCACAC GCCCCCGAACT ACCCACAAAC GCTACCCCCAAC GCCACCACAC GCCACCACAC GCCACCACAC GCCACCACCACAC GCCACCACCACAC GCCACCACAC GCCACCACAC GCCACCACCACAC GCCACCACCACAC GCCACCACCACAC GCCACCACCACAC GCCACCACCACAC GCCACACCACAC GCCACCACAC GCCACCACCACAC GCCACCACCACCACAC GCCACCACAC GCACCACCACAC GCCACCACAC GCCCCCCCACCACAC GCCACCACAC GCCACCACAC GCCCCCCCC	CAACCAGCCC	GACACGACAA	GTGTGTGCTG	GCCAGGTGTA	AAGCCATTGA	AATGTCCTGG
GTGGTCAAGT CCCGGTTCCC GAACGGACCG AGGCGTTGA ATGTGCACCT GCGACCAGATG CACCAGATCA CCCGGTTCCC GAACGGACCG AAGGCGTTGA ATGTGCACCT GCTGGTCACC GAACGGACCG AAGGCGTTGA ATGTGCACCT GCTGGTCACC GAACGGACCG AAGGCGTTGA ATGTGCACCT GCTGGTCACC GAACGGACCG AAGGCGTTGA ATGTGCACCT GCTGGTCACC GAACGGACCG AAGGCGTTGA ATGTGCACCT GCGATGCTTC CGACAGAGG CCCACGAGA GCCCACAGAG GCTCACCCGAG GCTACCCGAC GCCACGGAC GCCCAGAGAG GCCCCTGACC GCCCAGAGAG GCCCCTGACC GCCCAGAGAG ACCCACAAAGTT ACCCACAAAGT TACGTGTTCA GCCCCAGAGAGT GCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCAGAGAGT GCCCCAGAGAGT GCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCCAGAGAGT GCCCAGAGAGT GCCCAGAGAGT GCCCAGAGAGT GCCCAGAGAGT GCCCAGAGAGAGAGAAAAAAAAAA	GCTTGTACAC	GAGAGAGACA	AATGAACTGG	CTCTAGCCTC	CAGCCTTGCT	GACTCCTTTG
GCTGTCATTC CGACAGTAGG TCATGAGGAC CTACCCCGAG TACCACAAAC GGTACCCGAC CGCTAGGAAG 4150 ACTCCAGGAT TGGTTACAGT TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGGAGTCCTA TGAGGTCCTA TACCACAAAC TTACTGTGCG 4210 ACCCAGAGTTA TACCACAAAGT TACCACAAAGT TACCACAAAGT TACCACAAAGT TACCACAAAGT TACCACAAAGT TACCACAAAGT TACACACAAAGT TACACACAAAGT TACACACAAAGT TACACACAAAGT TACACACAAAGT TACACACAAAGT TACACACAAAGT TACACACACAAAC TTACACACACAC TTACACACACA	CGACCAGATG	TACACGTGGA	TTCCGCAACT	CTTGCCTGGC	GGGCCAAGGG	STEGTCAAGT
ACCAATGTCA TGGTTACAGT TGAGGTCCTA TACCACAAGT TACCACAACA TACCACACACACACACACACACACACA	GCGATCCTTC	CCATGGGCTG	ATGGTGTTTG	GATGGGGCTC	AGTACTCCTG	GCTGTCATTC
ATGCACAAGT CCCGGATGTA CAGCCAGTGT GTCCGAATGA GGCACCTCTC TCAAGAGTTT TACGTGTTCA GGGCCTACAT GTCGGTCACA CAGGCTTACT CCGTGGAGAG AGTTCTCAAA 4270 4280 4290 4300 4310 4320 ACTCTCAGC CCTACCGAGG TTTAGTGGGG GGTCCTTAAG GACACGTACT TTCGTGACGA TGAGAAGTCG TTAGTGGGG GGTCCTTAAG GACACGTACT TTCGTGACGA TGAGAAGTCG TGAGAAGTCA AAATTCTTTG ATGAACTTCG TAATAAGGTC ACCTACCGA CTTTTTAGTT TTTAAGAAAC TACTTGAAGC TTACTTGATG AGCTACCTA CATTGCATGC AAAAGAAAAAAAAAA	TGAGTACCGC	TGGTTTTCAA	GCCCCTGATC	GCTCTACTTC	ACTCCAGGAT	ACCAATGTCA
GGATGGCTCC AAATCACCCC CCAGGAATTC CTGTGCATGA AAGCACTGCT TCGTGACGA TTTAGTGGGG GGTCCTTAAG GACACGTACT TTCGTGACGA TGAGAAGTCG 430	TCAAGAGTTT	GGCACCTCTC	GTCCGAATGA	CAGCCAGTGT	CCCGGATGTA	ATGCACAAGT
ATTATTCCAG TGGATGGGCT GAAAAATCAA AAATTCTTTG ATGAACTTCG AATGAACTAC TAATAAGGTC ACCTACCGA CTTTTTAGTT TTTAAGAAAC TACTTGAAGC TTACTTGATG 4390 4400 4410 4420 4430 4440 ATCAAGGAAC TCGATCGTAT CATTGCATGC AAAAGAAAAA ATCCCACATC CTGCTCAAGA TAGTTCCTTG AGCTAGCATA GTAACGTACG TTTTCTTTTT TAGGGTGTAG GACGAGTTCT 4450 4460 4470 4480 4490 4500 CGCTTCTACC AGCTCACCAA GCTCCTGGAC TCCGTGCAGC CTATTGCGAG AGAGCTGCAT GCGAAGATGG TCGAGGACCTG AGGCACGTCG GATAACGCTC TCTCGACGTA	ACTCTTCAGC TGAGAAGTCG	AAGCACTGCT TTCGTGACGA	CTGTGCATGA GACACGTACT	CCAGGAATTC GGTCCTTAAG	AAATCACCCC TTTAGTGGGG	GGATGGCTCC
ATCAAGGAAC TCGATCGTAT CATTGCATGC AAAAGAAAAA ATCCCACATC CTGCTCAAGA TAGTTCCTTG AGCTAGCATA GTAACGTACG TTTTCTTTTT TAGGGTGTAG GACGAGTTCT 4450 4460 4470 4480 4490 4500 CGCTTCTACC AGCTCACCAA GCTCCTGGAC TCCGTGCAGC CTATTGCGAG AGAGCTGCAT GCGAAGATGG TCGAGTGGTT CGAGGACCTG AGGCACGTCG GATAACGCTC TCTCGACGTA	AATGAACTAC TTACTTGATG	ATGAACTTCG TACTTGAAGC	AAATTCTTTG TTTAAGAAAC	GAAAAATCAA	TGGATGGGCT	ATTATTCCAG
CGCTTCTACC AGCTCACCAA GCTCCTGGAC TCCGTGCAGC CTATTGCGAG AGAGCTGCAT GCGAAGATGG TCGAGTGGTT CGAGGACCTG AGGCACGTCG GATAACGCTC TCTCGACGTA	CTGCTCAAGA	ATCCCACATC	AAAAGAAAAA	CATTGCATGC	TCGATCGTAT	ATCAAGGAAC
	AGAGCTGCAT	CTATTGCGAG	TCCGTGCAGC AGGCACGTCG	GCTCCTGGAC CGAGGACCTG	AGCTCACCAA TCGAGTGGTT	CGCTTCTACC

FIGURE 4 (page 6 of 6)

4510	4520	4530	4540	4550	4560
CAGTTCACTT	TTGACCTGCT	AATCAAGTCA	CACATGGTGA	GCGTGGACTT	TCCGGAAATG
GTCAAGTGAA	AACTGGACGA	TTAGTTCAGT	GTGTACCACT	CGCACCTGAA	AGGCCTTTAC
4570	4580	4590	4500	4610	4620
ATGGCAGAGA	TCATCTCTGT	GCAAGTGCCC	AAGATCCTTT	CTGGGAAAGT	CAAGCCCATC
TACCGTCTCT	AGTAGAGACA	CGTTCACGGG	TTCTAGGAAA	GACCCTTTCA	GTTCGGGTAG
4630	4640	4650	4660	4670	4680
TATTTCCACA	CCCAGTGAAG	CATTGGAAAC	CCTATTTCCC	CACCCCAGCT	CATGCCCCCT
ATAAAGGTGT	GGGTCACTTC	GTAACCTTTG	GGATAAAGGG	GTGGGGTCGA	GTACGGGGGA
4690	4700	4710	4720	4730	AACCCCTTAA
TTCAGATGTC	TTCTGCCTGT	TATAACTCTG	CACTACTECT	CTGCAGTGCC	
AAGTCTACAG	AABACGGACA	ATATTGAGAC	GTGATGAGGA	GACGTCACGG	
4750	4760	4770	4780	4790	GACCCGAAAA
TCCTCTATTG	ATGTACAGTC	TGTCATGAAC	ATGTTCCTGA	ATTCTATTTG	
AGGAGATAAC	TACATGTCAG	ACAGTACTTG	TACAAGGACT	TAAGATAAAC	
4810 TTTTTCTCTT AAAAAGAGAA	4820 TCTCTCCTTT AGAGAGGAAA	4830 CTTTTTCTTC GAAAAAGAAG	48,40 TTCCCTCCCT AAGGGAGGA	ATCTAACCCT	666 FACCO F
4870	4880	4890	4900	TGAATGGTGT	4920
CTTCAGACTT	TGCTTCCCAT	TGTGGCTCCT	ATCTGTGTTT		TGTATGCCTT
GAAGTCTGAA	ACGAAGGGTA	ACACCGAGGA	TAGACACAAA		ACATACGGAA
4930 TAAATCTGTG ATTTAGACAC	4940 ATGATCCTCA TACTAGGAGT	TATEGCCCAG	TGTCAAGTTG	TGCTTGTTTA	CAGCACTACT
4990	5000	5010	5020	GGAAGTTTAG	5040
CTGTGCCAGC	CACACAAACG	TTTACTTATC	TTATGCCACG		AGAGCTAAGA
GACACGGTCG	GTGTGTTTGC	AAATGAATAG	AATACGGTGC		TCTCGATTCT
5050 TTATCTGGGG AATAGACCCC	5060 AAATCAAAAC TTTAGTTTTG	AAAAAACAAG	CAAACAAAAA	AAAAA	

FIGURE 5 (page 1 of 5)

·	J	1			
		40 TACATGGCAA	30 CGCCTATGTG	20 CAAAATTGAG	10 GAGCTCTGGA
	110 GATGAGAAAT	100 TGAGAGTCTG	90 ATTTTGCCTT	80 TGTCTGGGTG	70 TTTACCTGCT
		160 AAGAGGGTAG	150 AAAGGCAGAG	140 AGACAGGAAG	OE1 COTTAACOOA
		220 TGCCACGAGG		200 TCCTAGAGCA	190 GGCTGAGGGT
			270 CAGCTATCTG	260 GTTTCAGCAT	250 GAACTCTAAG
	350 TCAGTCCTGA	340 CGCGCTCTTA	330 CTCCCATCTG	320 CTCTCCCACT	310 TTGTAGGAGA
		400 TCCTTTTCNT		380 GGAGCNAGGT	370 TGGCNAGCCA
			450 NAACCAAATT	440 TTGGNCTTNG	430 GNTTTTTAGA
540 TCCTCCAGGG			510 AGGAAAGCAG	500 ACCTTGGTTT	490 T66C6CCTAA
600 CCAAAGCNAC	590 ACTTGTTTCT	580 GTGCGCCAGC	570 CCTCGCCCAC	560 CCTCTCCT6C	550 CTAGAGCTAG
	650 GAAAGGGGAG	640 GGGAGAAAAG	026 61686888	620 TTAGCGCGCG	610 TAGGCAGGCG
	710 GACCCGACTC	700 GTGGGGGCGG	690 GGCCGGCCNG	680 AAGGCAAGGA	670 AGGAGGTGGG
		760 CTCCGAGATC		740 TCTCCACCTC	730 TTGCATTTGC
		820 AGGCAGAGGA	810 GCAAGCCCAG	800 ACGGTCCGGA	790 GAGAGCGGGA
900 CAGCCCCAGC	890 CGCACCACGC	880 AGCCGAAGGA	870 GCTGTACAGN	860 CCGCTCCAGT	850 CCCNAGCTAG
	950 AGCCGCCGCC		930 C6CCTCTT6C	920 CGACAGCNAA	910 CCGGCTCCAG
1020 AAGGAAAGTG	1010 CGGAGGAAGC	1000 BCTAAAGACT	990 TTTAAAAGCT	980 CGGTGAAGTT	970 CTTTCCTCTT
1080 CCCCACCCT	1070 ACCCCGCCTC	1060 CCTCCTCTCC	1050 CCTTTGTCCT	1040 CTGACGGCTG	1030 CCTGGTAGGA
1140 CTCTCAGCCA					
1200 AGCGNTGNCA				1160 CCACCCTTCT	
1260 AGCTGCACAT	1250 GGGCGAGNCT	1240 ÆGCTGCGAGC	1230 AACTCCCTTT	1220 GCAGAGAGGT	1210 GNCCGAGTTT

FIGURE 5 (page 2 of 5)

1290 . TGCHAAGAAG GCTCTTAGGA GCAGGCGACT GGGGAGCGGC TTCAGCACTG CAGCCACGAC CNGCCTGGTT AGGCTGCACG CGGAGAGAAC CCTCTGTTTT CCCCCACTCT CTCTCCACCT CCTCCTGCCT TCCCCACCC GAGTGCGGAG CCAGAGATCA AAAGATGAAA AGGCAGTCAG 1450 1460 1470 1480 1490 1500 STOTTCASTA SCCAAAAAC AAAACAAACA AAAACAAAAA AGCCGAAATA AAAGAAAAAB ATAATAACTC AGTTCTTATT TGCACCTACT TCAGTGGACA CTGAATTTGG AAGGTGGAGG ATTITETTIT TITCTTTTAA GATCTGGGCA TETTTTGAAT CTACCCTTCA AGTATTAAGA GACAGACTGT GAGCCTAGCA GGGCAGATCT TGTCCACCGT GTGTCTTCTT CTGCACGAGA CTTTGAGGCT GTCAGAGCGC TTTTTGCGTG GTTGCTCCCG CAAGTTTCCT 1CTCTGGAGC TTCCCGCAGG TGGGCAGCTA GCTGCAGCGA CTACCGCATC ATCACAGCCT GTTGAACTCT TOTGAGGAGG AGAASGGGGG GCGGGGTAAG GGAAGTAGGT GGAAGATTCA GCCAAGCTCA 650 ATS GAA GTG CAG TTA GGG CTG GGA AGG GTC TAC CCT CGG CCG CCG TCC AAG ACC T+C Tet Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr DBA BBA BBT TTD DAG AAT DTG TTD DAG AGD BTG DGC BAA GTG ATD DAG AAD DDG BBS DSS Arg Gly Ala Phe Gln Ash Leu Phe Gln Ser Val Arg Glu Val Ile Gln Ash Pro Gly Pro ASS CAC DOA GAG GOD GOG AGO GOAGO GOD AGO TTG CTG CTG CAG CAG Ary His Pro Glu Ala Ala Ser Ala 🐴 🛕 Pro Pro Gly Ala Ser Leu Leu Leu Gln 51-1 CAG CAG GAG ACT AGC CCC AGG CAG CAG CAG CAG CAG GGT GAG GAT GGT TCT CCC Gin Gin Gin Glu Thr Ser Pro Arg Gin Gin Gin Gin Gin Gin Gly Glu Asp Gly Ser Pro CAA GCC CAT CGT AGA GGC CCC ACA GGC TAC CTG GTC CTG GAT GAG GAA CAG CAA CCT TCA Gin Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln Gln Pro Ser CAS CCG CAG TCG GCC CTG GAG TGC CAC CCC GAG AGA GGT TGC GTC CCA GAG CCT GGA GCC 61n Fro 61n Ser Ala Leu 61u Cys His Pro 61u Arg 61y Cys Val Pro 61u Pro 61y Ala GCC GTG GCC GCC AGC AGG GGG CTG CCG CAG CAG CTG CCA GCA CCT CCG GAC GAG GAT GAC Ala Val Ala Ala Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp

The second second section is the major of the second

FIGURE 5 (page 3 of 5) -- --

TO BET BEC DEA TOO ADD TIG TOO DIG DIG BEC DOD ACT TIC COD GGC TTA AGD AGD TGD Sen Ale Ale Fre Ser The Leu Ser Leu Leu Gly Pro The Phe Pro Gly Leu Ser Ser Cys 2430 THE GET GAD CIT ANA GAD ATE CIG AGE GAD GED AGE ACC ATG CAA CIC CIT CAG CAA CAG Ser Ale Asp Leo Lys Asp 11e Leo Ser Glo Ale Ser Thr Met Gln Leo Leo Gln Gln Gln 2490 DON LOS BAN GUA GIA TOC BAN GGO AGO AGO AGO AGO AGA GCG AGG GAG GCC TCG GGG GCT Gin Gin Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala 2550 TYC ACT ICC ICC AAG GAC AAT TAC TIN 656 GGC ACT ICG ACC ATT ICT GAC AAC GCC AAG In a library Ser Lys Asp Ash Tyr Leu Gly Gly Ihr Ser Thr Ile Ser Ash Ash Ala Lys 2610 GAG (18 16) AAR GCA G16 10G G16 TCC A1G GGC CTG GGT GTG GAG GCG TTG GAG CAT CTG (to tro tys tys Ale Val Ser Val Ser Met Sly Leu Gly Val Glu Ala Leu Glu His Leu 2670 PST CCA GGG GAA CAG CIT CGG GGG GAT TGC ATG TAC GCC CCA CTT TTG GGA GTT CCA CCC Ser Pro Gly Glo Glo Leo Ang Gly Asp Cys Met Tyr Ala Pro Leo Leo Gly Val Pro Pro 2730 503 616 607 000 A01 007 167 600 00A 116 600 GAA 160 AAA 667 TCT CTG CTA GAC GAC Als Val Ala Pro The Fro Cys Ala Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp 2750 2820 AND GCA GGC AAR AGC ACT GAA GAT ACT GCT GAG TAT TCC CCT TTC AAG GGA GGT TAC ACC Ser Ala Gly Lvs Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr 2850 ANA GRE CTA GAN REÉ GAG AGC CTA GRE TEC TOT GRE AGC GCT GCA GCA GGG AGC TCC GGG tys Glv Leo Glo Gly Glo Ser Leo Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly 2910 ACA ETT BAA CTG CCG TCT ACC.CTG TCT CTC TAC AAG TCC GGA GCA CTG GAC GAG GCA GCT The less file thee Fire Ser Thir Less Ser Less Tyr Lys Ser Gly-Ala Less Asp Glu Ala Ala 2970 GOD TAD CAS AST DBD GAD TAD TAD AAC TIT CCA CTG GCT CTG GCC GGA CCG CCC CCT Ale Tyr Glm Ser Arg Asp Tyr Tyr Asm Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro 3060 3030 ECO COS CET COO CAT COO CAC GOT CGC ATC AAG CTG GAG AAC CCG CTG GAC TAC GGC AGC Pro Pro Pro Pro His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser 3090 GOO TES SES SET CAT GOS SES CAGTED CONTRACT SES SES SES ASC CTS CAT GGC GCG Mis Top Ale Ala Ala Mia Ala Gin Cys Arg Mr Gly Asp Leu Ala Ser Leu His Gly Ala 3150 SET GOA GOG GEN DOD BET TOT GEG TON DOD TOA GOD GOD GOT TOO TOA TOO TGG CAC ACT Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser Trp His Thr 3210

they Phe Thr Ale Glu Glu Gly Glu Ley lyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly

FIGURE 5 (page 4 of 5)

3270 3330 GCT GTA GCC CCC TAC GGC TAC ACT CGG CCC CCT CAG GGG CTG GCG GGC CAG GAA AGC GAC Ala Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp 3390
TIC ACC GCA CCT GAT GTG TGG TAC CCT GGC GGC ATG GTG AGC AGA GTG CCC TAT CCC AGT Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro Tyr Pro Ser 3450 3480 CCC ACT TGT GTC AAA AGC GAA ATG GGC CCC TGG ATG GAT AGC TAC TCC CGG GAA CCT TAC Fro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp Ser Tyr Ser Arg Glu Pro Tyr 3510 GGG GAC ATG CGT TTG GAG ACT GCC AGG GAC CAT GTT TTG CCC ATT GAC TAT TAC TTT CCA Gly Asp Met Arg Leu Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro 3570 CCC CAG AAG ACC TGC CTG ATC TGT GGA GAT GAA GCT TCT GGG TGT CAC TAT GGA GCT CTC Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu 3630 ACA TET EGA AGC TEC AAG ETC TTC TTC AAA AGA ECC ECT GAA EGE AAA CAG AAG TAC CTG Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu 3690 TGC GCC AGC AGA AAT GAT TGC ACT ATT GAT AAA TTC CGA AGG AAA AAT TGT CCA TCT TGT Dys Ala Ser Arg Ash Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Ash Cys Pro Ser Cys 3750 CGT CTT CGG AAA TGT TAT GAA GCA GGG ATG ACT CTG GGA GCC CGG AAG CTG AAG AAA CTT Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu 3810 GGT AAT CTG AAA CTA CAG GAG GAA GGA GAG GCT TCC AGC ACC ACC ACC ACT GAG GAG Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu ACA ACC CAG AAG CTG ACA GTG TCA CAC ATT GAA GGC TAT GAA TGT CAG CCC ATC TTT CTG Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu AAT STC CTG GAA GCC ATT GAG CCA GGT GTA GTG TGT GCT GGA CAC GAC AAC CAG CCC Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn Gln Pro GAC TCC TTT GCA GCC TTG CTC TCT AGC CTC AAT GAA CTG GGA GAG AGA CAG CTT GTA CAC Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His 4050 GTG GTC AAG TGG GCC AAG GGC TTG CCT GGC TTC CGC AAC TTA CAC GTG GAC GAC CAG ATG Val Val Lys Trp Ala Lys Gly Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met 4110 GCT GTC ATT CAG TAC TCC TGG ATG GGG CTC ATG GTG TTT GCC ATG GGC TGG CGA TCC TTC Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe

FIGURE 5 (page 5 of 5)

ACC AAT GTC AAC TCC AGG ATG CTC TAC TTC GCC CCT GAT CTG GTT TTC AAT GAG TAC CGC Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg ATG CAC AAG TCC CGG ATG TAC AGC CAG TGT GTC CGA ATG AGG CAC CTC TCT CAA GAG TTT Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe GGA TGG CTC CAA ATC ACC CCC CAG GAA TTC CTG TGC ATG AAA GCA CTG CTA CTC TTC AGC Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser ATT ATT CCA GTG GAT GGG CTG AAA AAT CAA AAA TTC TTT GAT GAA CTT CGA ATG AAC TAC Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr ATC AAG GAA CTC GAT CGT ATC ATT GCA TGC AAA AGA AAA AAT CCC ACA TCC TGC TCA AGA Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg CGC TTC TAC CAG CTC ACC AAG CTC CTG GAC TCC GTG CAG CCT ATT GCG AGA GAG CTG CAT Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His CAG TTC ACT TTT GAC CTG CTA ATC AAG TCA CAC ATG GTG AGC GTG GAC TTT CCG GAA ATG Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met ATG GCA BAG ATC ATC TCT GTG CAA GTG CCC AAG ATC CTT TCT GGG AAA GTC AAG CCC ATC Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile TAT TTC CAC ACC CAG TGA AGC ATT GGA AAC CCT ATT TCC CCA CCC CAG CTC ATG CCC CCT Tyr Phe His Thr Gln End . TTCAGATGTC TTCTGCCTGT TATAACTCTG CACTACTCCT CTGCAGTGCC TTGGGGAATT

TCCTCTATTG ATGTACAGTC TGTCATGAAC ATGTTCCTGA ATTCTATTTG CTGGGCTTTT CTTCAGACTT TGCTTCCCAT TGTGGCTCCT ATCTGTGTTT TGAATGGTGT TGTATGCCTT TAAATCTGTG ATGATCCTCA TATGGCCCAG TGTCAAGTTG TGCTTGTTTA CAGCACTACT CTGTGCCAGC CACACAACG TTTACTTATC TTATGCCACG GGAAGTTTAG AGAGCTAAGA TTATCTGGGG AAATCAAAAC AAAAAACAAG CAAACAAAAA AAAAA

FIGURE 6 (page 1075)

F 1 1

	10	2 0	30	40	50	60
AATTOS	REGARGETCS	AECAAACTAG	GAAACTAASE	A I BGAGA I CC	TABBABBIG	ILLA
тесстс	70 GAAAGGAGCD	90 CACCAAAGAT	90 GAACTGTTGC	100 ATTTGCTTTS		120 CGCC
	130	140	150	160	170	180
COCTOB	BAGATCCCTA	66ASICAGOC	TGCT666ASA	ACCAGAGGGT	CCGGAGCAAA	DOTE
SABBOT	190 GAGAGGGCAT	200 CA6A3666AA	210 AABACTGAGT	220 TABCCACTSC	250 AGTGCCATAC	240 AGAA
GCTTAA	250 IGGGACATACC	260 AC3CC4GCCC	270 CAGCCCAGCG	280 ACASCCAACG	290 COTGTTGCAG	300 AGCG
GCGGCT	310 TCGAAGCC3C	320 CGCCCAGAAG	330 2760027770	540 CTCTTCGGTG	350 AASTTTCTAA	360 AAGC
	370	380	390	400	410	420
TGCGGF	AGACTOGGAS	GAAGCGAAGA	AASTGTCEGS	TAGGACTACG	ACTOCCTTTG	TOOT
сетаес	430 YESTACSECT	440 ACCCCTCCTG	450 GGTOCCCTCT	460 CCCTGAGCGG	470 ACTAGGCAGG	480 CTTC
OTGGCC	490 :AGCCCTCTCC	500 CCTACACCAC	510 CAGCTCTGCC	520 ASCCAGTTTG	530 CACAGAGGTA	. 540 ACTO
COTTIE	550 GCTGAAAGCA	560 GACGAGCTTG	570 TTGCCCATTG	580 GAAGGGAGGC	590 TTTT666460	600 CCA5
AGACTE	610 AGGAGJAADA	620 GCACGCTGGA	630 GAGTCCCTGA	640 TTCCAGGTTC	650 TOCCOCOTGO	660 ACCT
CCTACT	670 GCCCGCCCCT	680 CACCCTGTST	690 GTGCAGCTAS	700 AATTGAAAAG	710 ATGAAAAGAC	720 AGTT
666601	720 TCAGTAGTCS	740 PAAGCARAAC	750 AAAABCAAAA	760 (AGAAAACAAA	770 AASAAAAT AG	780 CCCA
GTTCTT	790 MITTTBCACCT	800 GCTTCAGTGS		920 TGGAAABCAS	SSO PARTITICO	840 TTCC
րորոն	950 HOAAGOTTIG	860 ABCATOTTT	-870 AATOTETTOT	- 580 TITAAAATT	890 'AGGGADAAAC	900 TGTG

1. 1

FIGURE 6 (page 2 of 5)

FIGURE 6 (page 3 of 5)

1 1 ACCATATCTGACAGTGCCAAGGAGTTGTGTAAAGCAGTGTCTGTGTCCATGGGGTTGGGT Thr IleSerAspSerAlaLysGluLeuCysLysAlaValSerValSerMetGlyLeuGly GTGCAAGCACTGGAACATCTGAGTCCAGGGGGAGCAGCTTCGGGGGCGACTGCATGTACGCG ValGluAlaLeuGluHisLeuSerProGlvGluGlnLeuArgGlyAspCysMatTyrAla TESCIDEIGESAGGICCACCEGCGICGICGICCACICCITSIGCGCCICITGGCCGAAIGC SenteuleuGlyGlyProProAlaValArgProThrProCysAlaProLeuAlaGluCys AMAGGTETTTCCCTGGACGAAGGCCCGGGCAAAGGCACTGAAGAGACTBETGAGTATTCC LysSlyLeuSerLeuAspGluGlyProGlyLysSlyThrOluGluThrAlaGluTyrSer TETTTCAAGGGAGGTTACGCCAAAGGGTTGGAAGGTGAGAGTCTBGGCTGCTCTGGCAGC SerPheLysGlyGlyTyrAlsLysGlyLeuGluGlyGluSerLeuGlyCysSerGlySer AGTGAAGCAGGTAGCTCTGGGACACTTGAGATCCCGTCCTCACTGTCTCTGTATAAGTCT SerGluAlaGlySerSerGlyThrLeuGluIleProSerSerLeuSerLeuTyrLysSer GlyAlaValAspGluAlaAlaAlaTymGlnAsnArgAspTymTvmAsnPheProLeuAla CTGTCDEGGCCGCCGCACCCCCCGCCCCTACCCATCCACACGCCCGCATCAAGCTGGAG LeuSsrGlyProProHisProProProProThrHisProHisAlaArgIleLysLeuGlu AADDDSTOGGACTACGGCAGCGCCTGGGCTGCGGCGGCGCGCAATGCCGCTATGGGGAC AshProSerAspTyrGlySerAlaTrpAlaAlaAlaAlaAlaAlaSlnCysArgTyrGlyAsp TTGGCTABCCTACATGGAGGGAGTGTAGCCGGACCCAGCACTGGATCGCCCCCAGCCACC LeuAlaSerLeuHisGlyGlySerValAlaGlyFroSerThrGlySerFroFroAlaThr GCCTCTTCTTCCTGGCATACTCTCTTCACAGCTGAAGAAGGCCAATTATATGGGCCAGGA AlaSerSerSerTrpHisThrLeuPheThrAlaGluGluGlyGlnLeuTyrGlyProGly CACABRAGO PARCARTAGO CAAGOSATROTAGGO COTATAGO CACAGO CACAGO CAAGO C GlyGlvGlyGlyGlySerSerSerFroSerAspAlaGlyProValAlaFroTyrGlyTyrThr 25.60 COSCICECTEAGGGOCTGGCÀAGCCAGGAGGGTGACTTCTCTGCCTCTGAAGTGTBGTAT ArgPrcProGin6lyLeuAlaSerGin3luGlyAspPheSerAlaSerGiuValTrpTyr

CCTSSTSGAGTTGTGAACAGAGTCCCCTATCCCAGTCCCAGTTGTGTTAAAAGTGAAATG ProGlyGlyValValAsnArgValFroTyrFroSerFroSerCysValLysSerGludet

GSACCTTGGATGGAGAACTACTCCGGACCTTATGGGGACATGCGTTTGGACASTACCAGG @)vProTroMotGluAsnTyrSerGlyProTyrGlyAspMetArgLeuAspSerThrArg

FIGURE 6 (page 4 of 5)

J. 3						
GACCACE	TITTACCCA			DCAGAAGACC		
2	2770	2780	2790	2600 2600 FTGTGGCAGC	2910	2820
Asp5luA	laSerGlvC			roys6lySer(-2360		
AAAAGAG	CTGCGGAAG	IGGAAACAGAA	STATCTATE	TGCCASCAGA sAlaSerArga	AATGATTSCA	CATT
GATAAAT				2920 TOTOOGGAAA gLeuArqLyg		
ATGACTO	TGGGAGCTC			2980 AAATCTCAAAI /AsnLeuLysl		
GAAAACT				3040 ATCCCAGAAGA SerG1nLys!		
ATTGAAG	GCTATGAAT	3080 GTCAACCTAI YBG]nProIl	3090 "CTTTCTTAA" ePheLeuAsr	3100 TGTCCT6GAA(WalleuGluA	3110 3CCATTSAGC AlalleGluPy	3120 CAGGA COGly
втветет				3160 FTCCTTTGCT0 SerPheAla		
CTCAACG	ASCTTEECE			3220 3GTCAASTGG(ValLysTrp/		
BECTTOO	GCAACTTGC			3280 AGTCATTCAGI aVallleGlni		
CTGATGG	TATTTGCCA			SB40 TAATGTCAAC 'AshValAsh9		
TTTGCAC	CTGACCTGG			- 3400 SCACAAGTOTE tHisLysSer		
TGIGTER	GBHT GABSC	ACCTITOTO		3440 ATGGCTCCAGA /TrpLeuGlnl		
TTOOTGT	GCATGAAAG	CACTGCTACT	3510 CTTCAGCATT :uPheSprIle	3520 ATTCCAGTG0 PileProVal4	3530 SATGEGETGAA Aspelyteuty	3540 TAAAf naAay
			3570 GAACTACATO	3580	5590°	3600
CAAAAAAT	151116416	HUCI I ORHU:	CHACHICHIC	AMMONHMENT I	am i Guum i Gh	TUNE

 ${\tt GlinLysPhePheAsp@luLeoArgMetAsnTyrIleLysGluLeoAspArgIleIleAla}$

FIGURE 6 (page 5 of 5)

3510 3520 3630 3640 3650 3660 TGCAAAAGAAAAATCCCACATCCTGCTCAAGGCGCTTCTACCAGCTCACGAAGGTCCTG CysLysArgLysAsnProThrSerCysSerArgArgPheTyrG1nLeuThrLysLeuLeu

3670 3680 3690 3700 3710 3720
GATTCTGTGCAGCCTATTGCAAGAGAGCTGCATCAATTCACTTTTGACCTGCTAATCAAG
AspSerValG1:ProIleAlaArgGluLeuPisG1:PheTbcPheAspLeuLeuIleLys

2790 2800 3810 2820 2830 3840 CCCÄAGATCCTTTCTSSGAAASTCAGCCCATGTATTTCCACACACAGTGAAGATTTGGAA ProLysIleLeuSerGlyLysValSerProCysIleSerThrHisSerGluAspLeuGlu

3850 3860 3870 3880 3890 3900 CCTAATACCCAAACCCACCTGTTCCCTTTTCAGATGTCTTCTGCCTGTTATATAACTCTG ProAsnThr3lnThrHisLeuPheProPheGlnMetSerSerAlaCysTyrIleThrLeu

3710 3720 3730 3740 3750 2760 CACTACTTCTCTGGGCATGGGCCTTGGGGGAAATTCCTCTACTGATGTACAGTCTGTCATGHisTyrPheSerGlyMetGlyLeuGlyGlyAsnSerSerThrAspValGlnSerValMet

4090 4100 4110 4180 4130 4140 TTTGAGTTTTGTGTGTGTGTGTGTGTGTGTGTGTGAGTTGTGTGTGTGTGAGTTGAGTTTGTGTGGCCCAGTGTCAACT PheGloPheCysCysIleSerSerSerLeuEnd

4150 4160 4170 4180 4190 4200 6T6CTTGTTTATAGCACTGTGTGTGCCAACCAAGCAAATSTTTACTCACCTTATGCC

4270 4280 CCASAAAAAAAAAAAAAAAAACCGAATTC

Figure 7. Frozen section of rat ventral prostate stained with antibodies (AR-52-3-p) to the AR peptide NH₂-Asp-His-Val-Leu-Pro-Ile-Asp-Tyr-Tyr-Phe-Pro-Gln-Lys-Thr in a dilution of 1 to 3000 using the avidin-biotin peroxidase technique. Androgen receptor is indicated by brown staining of nuclei in epithelial cells. Immuno-staining was performed as previously described (60).

Restriction Fragment Length Polymorphism in the Human Androgen Receptor Gene

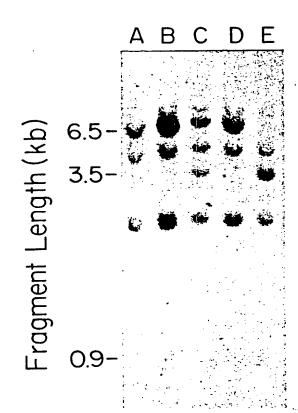


FIGURE 9

Southern Blot Analysis of Complete Androgen Insensitivity Syndrome Patients

